



SEQUENCE LISTING

<110> Clark, Janet

<120> METHOD FOR IDENTIFYING COMPOUNDS THAT
AFFECT EXPRESSION OF TRYPTOPHAN HYDROXYLASE ISOFORM 2

<130> 21487YP

<140> 10/576,807

<141> 2006-04-21

<150> PCT/US2004/34619

<151> 2004-10-20

<150> 60/514,268

<151> 2003-10-24

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 447

<212> PRT

<213> Mus musculus

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Glu Arg Gly Arg Val Thr Leu Ile Phe Ser Leu Glu Asn Glu Val Gly
20 25 30
Gly Leu Ile Lys Val Leu Lys Ile Phe Gln Glu Asn His Val Ser Leu
35 40 45
Leu His Ile Glu Ser Arg Lys Ser Lys Gln Arg Asn Ser Glu Phe Glu

50 55 60
 Ile Phe Val Asp Cys Asp Ile Ser Arg Glu Gln Leu Asn Asp Ile Phe
 65 70 75 80
 Pro Leu Leu Lys Ser His Ala Thr Val Leu Ser Val Asp Ser Pro Asp
 85 90 95
 Gln Leu Thr Ala Lys Glu Asp Val Met Glu Thr Val Pro Trp Phe Pro
 100 105 110
 Lys Lys Ile Ser Asp Leu Asp Phe Cys Ala Asn Arg Val Leu Leu Tyr
 115 120 125
 Gly Ser Glu Leu Asp Ala Asp His Pro Gly Phe Lys Asp Asn Val Tyr
 130 135 140
 Arg Arg Arg Arg Lys Tyr Phe Ala Glu Leu Ala Met Asn Tyr Lys His
 145 150 155 160
 Gly Asp Pro Ile Pro Lys Ile Glu Phe Thr Glu Glu Glu Ile Lys Thr
 165 170 175
 Trp Gly Thr Ile Phe Arg Glu Leu Asn Lys Leu Tyr Pro Thr His Ala
 180 185 190
 Cys Arg Glu Tyr Leu Arg Asn Leu Pro Leu Leu Ser Lys Tyr Cys Gly
 195 200 205
 Tyr Arg Glu Asp Asn Ile Pro Gln Leu Glu Asp Val Ser Asn Phe Leu
 210 215 220
 Lys Glu Arg Thr Gly Phe Ser Ile Arg Pro Val Ala Gly Tyr Leu Ser
 225 230 235 240
 Pro Arg Asp Phe Leu Ser Gly Leu Ala Phe Arg Val Phe His Cys Thr
 245 250 255
 Gln Tyr Val Arg His Ser Ser Asp Pro Leu Tyr Thr Pro Glu Pro Asp
 260 265 270
 Thr Cys His Glu Leu Leu Gly His Val Pro Leu Leu Ala Glu Pro Ser
 275 280 285
 Phe Ala Gln Phe Ser Gln Glu Ile Gly Leu Ala Ser Leu Gly Ala Ser
 290 295 300
 Glu Glu Thr Val Gln Lys Leu Ala Thr Cys Tyr Phe Phe Thr Val Glu
 305 310 315 320
 Phe Gly Leu Cys Lys Gln Asp Gly Gln Leu Arg Val Phe Gly Ala Gly
 325 330 335
 Leu Leu Ser Ser Ile Ser Glu Leu Lys His Ala Leu Ser Gly His Ala
 340 345 350

Lys Val Lys Pro Phe Asp Pro Lys Ile Ala Cys Lys Gln Glu Cys Leu
 355 360 365
 Ile Thr Ser Phe Gln Asp Val Tyr Phe Val Ser Glu Ser Phe Glu Asp
 370 375 380
 Ala Lys Glu Lys Met Arg Glu Phe Ala Lys Thr Val Lys Arg Pro Phe
 385 390 395 400
 Gly Leu Lys Tyr Asn Pro Tyr Thr Gln Ser Val Gln Val Leu Arg Asp
 405 410 415
 Thr Lys Ser Ile Thr Ser Ala Met Asn Glu Leu Arg Tyr Asp Leu Asp
 420 425 430
 Val Ile Ser Asp Ala Leu Ala Arg Val Thr Arg Trp Pro Ser Val
 435 440 445

<210> 2

<211> 488

<212> PRT

<213> Mus musculus

<400> 2

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 20 25 30
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 35 40 45
 Lys Glu Pro Gly Lys Gly Asp Thr Thr Glu Ser Ser Lys Thr Ala Val
 50 55 60
 Val Phe Ser Leu Lys Asn Glu Val Gly Gly Leu Val Lys Ala Leu Arg
 65 70 75 80
 Leu Phe Gln Glu Lys His Val Asn Met Leu His Ile Glu Ser Arg Arg
 85 90 95
 Ser Arg Arg Arg Ser Ser Glu Val Glu Ile Phe Val Asp Cys Glu Cys
 100 105 110
 Gly Lys Thr Glu Phe Asn Glu Leu Ile Gln Leu Leu Lys Phe Gln Thr
 115 120 125
 Thr Ile Val Thr Leu Asn Pro Pro Glu Ser Ile Trp Thr Glu Glu Glu

130	135	140
Asp Leu Glu Asp Val Pro Trp Phe Pro Arg Lys Ile Ser Glu Leu Asp		
145	150	155
Arg Cys Ser His Arg Val Leu Met Tyr Gly Thr Glu Leu Asp Ala Asp		
165	170	175
His Pro Gly Phe Lys Asp Asn Val Tyr Arg Gln Arg Arg Lys Tyr Phe		
180	185	190
Val Asp Val Ala Met Gly Tyr Lys Tyr Gly Gln Pro Ile Pro Arg Val		
195	200	205
Glu Tyr Thr Glu Glu Glu Thr Lys Thr Trp Gly Val Val Phe Arg Glu		
210	215	220
Leu Ser Lys Leu Tyr Pro Thr His Ala Cys Arg Glu Tyr Leu Lys Asn		
225	230	235
Leu Pro Leu Leu Thr Lys Tyr Cys Gly Tyr Arg Glu Asp Asn Val Pro		
245	250	255
Gln Leu Glu Asp Val Ser Met Phe Leu Lys Glu Arg Ser Gly Phe Thr		
260	265	270
Val Arg Pro Val Ala Gly Tyr Leu Ser Pro Arg Asp Phe Leu Ala Gly		
275	280	285
Leu Ala Tyr Arg Val Phe His Cys Thr Gln Tyr Val Arg His Gly Ser		
290	295	300
Asp Pro Leu Tyr Thr Pro Glu Pro Asp Thr Cys His Glu Leu Leu Gly		
305	310	315
His Val Pro Leu Leu Ala Asp Pro Lys Phe Ala Gln Phe Ser Gln Glu		
325	330	335
Ile Gly Leu Ala Ser Leu Gly Ala Ser Asp Glu Asp Val Gln Lys Leu		
340	345	350
Ala Thr Cys Tyr Phe Phe Thr Ile Glu Phe Gly Leu Cys Lys Gln Glu		
355	360	365
Gly Gln Leu Arg Ala Tyr Gly Ala Gly Leu Leu Ser Ser Ile Gly Glu		
370	375	380
Leu Lys His Ala Leu Ser Asp Lys Ala Cys Val Lys Ser Phe Asp Pro		
385	390	395
Lys Thr Thr Cys Leu Gln Glu Cys Leu Ile Thr Thr Phe Gln Asp Ala		
405	410	415
Tyr Phe Val Ser Asp Ser Phe Glu Glu Ala Lys Glu Lys Met Arg Asp		
420	425	430

Phe Ala Lys Ser Ile Thr Arg Pro Phe Ser Val Tyr Phe Asn Arg Tyr
435 440 445
Thr Gln Ser Ile Glu Ile Leu Lys Asp Thr Arg Ser Ile Glu Asn Val
450 455 460
Val Gln Asp Leu Arg Ser Asp Leu Asn Thr Val Cys Asp Ala Leu Asn
465 470 475 480
Lys Met Asn Gln Tyr Leu Gly Ile
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<212> DNA

<213> Artificial Sequence

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<223> TPH2a riboprobe template

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atcaaaagcg aggacaagaa aagcggcaaa gagcccggca aaggcgacac cacagagagc 180
agcaagacag cagttgtgtt ctccttgaag aatgaagtt 219

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<211> 219

<212> DNA

<213> Artificial Sequence

<220>

<223> TPH2b riboprobe

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cgggtcccggc gaagaagttc tgaagtcgaa atcttcgtgg actgcgaatg tggcaaaacg 120
gaattcaatg agctcatcca gttgctgaaa tttcagacca ccattgtgac cctgaatccg 180
cctgagagca tttggacgga ggaagaagat ctcgaggat 219

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<212> DNA

<213> Artificial Sequence

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<223> TPH2c riboprobe

<400> 5

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gattctgctg tgccagaaga tcatcagcta cttggcagct taacacaaaa taaggctatc 120
aaaagcgagg acaagaaaag cggcaaagag cccggcaaag gcgacaccac agagagcagc 180
aagacagcag ttgtgttctc cttgaagaat gaagttggtg ggctggtgaa agcacttaga 240
ctattccagg aaaaacatgt caacatgctt catatcgaat ccaggcggtc ccggcgaaga 300
agtttctaagt cgaaatcttc gtggactgcg aatgtggcaa aacggaattc aatgagctca 360
tccagttgct gaaatttcag accaccattg tgaccctgaa tccgcctgag agcatttgga 420
cggaggaaga agatctcgag gatgtgccgt ggttcacctg gaagatctct gagttagaca 480
gatgctctca ccgagtcctc atgtacggca ccgagcttga tgccgaccat ccaggattta 540
aggacaatgt ctatcgacag aggaggaagt attttgtgga tgtggccatg ggctataaat 600
atggtcagcc cattcccagg gtcgagtaca cagaagaaga gactaaaact tggggtggtg 660
tgttccggga gctctccaaa ctctaccga ctcattgctt ccgggagtac ctgaaaaacc 720
tccccctgct gaccaagtac tgtggctaca ggggaagacaa cgtgccgcaa ctggaagacg 780
tctccatgtt tctgaaagag cgatctggct tcacagtg 818
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<210> 6

<211> 842

<212> DNA

<213> Artificial Sequence

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<223> TPH2-892 riboprobe

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tacccgaccc acgcctgcag ggagtacctc agaaacctcc ctttgctctc aaaatactgt 120
ggctatcggg aagacaacat cccgcaactg gaggatgtct ccaacttttt aaaagaacgc 180
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actggggtttt ccatccgtcc tgtggctggg tacctctcac cgagagattt tctgtcgggg 240
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actccagagc cagacacctg ccatgaactc ctaggccaag ttcctctctt ggctgaaccc 360
agttttgtct aattctccca agaaattggc ctggcttccc ttggagcttc agaggagaca 420
gttcaaaaac tggcaacgtg ctactttttc actgtggagt ttgggctgtg caaacaagat 480
ggacagctga gagtcttttg ggccggcttg ctttcttcca tcagtgaact caaacatgca 540
ctttctggac atgccaaagt caagcccttt gatcccaaga ttgcctgtaa acaggaatgt 600
ctcatcacga gcttccagga tgtctacttt gtatctgaga gctttgaaga tgcaaaggag 660
aagatgagag aatttgccaa gaccgtgaag cgcccgtttg gactgaagta caaccgtac 720
acacagagtg ttcaggttct cagagacacc aagagcataa ctagtgccat gaatgagttg 780
cggtagacct tgatgtcatc agtgatgccc tcgctagggt caccaggtgg cccagtgtgt 840
ga

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<210> 7

<211> 22

<212> DNA

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<223> Murine TPH2 forward primer mTPH2-514F

<400> 7

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<210> 8

<211> 21

<212> DNA

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<400> 8

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<210> 9

<211> 22

<212> DNA

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<223> Murine TPH2 reverse primer mTPH2-585R

<400> 9

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22

<210> 10

<211> 21

<212> DNA

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<223> Murine TPH2 reverse primer mTPH2-1344R

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<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Murine TPH2 probe mTPH2-565T

<400> 11

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27

<210> 12

<211> 26

<212> DNA

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<223> Murine TPH2 probe mTPH2-1292T

<400> 12

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26